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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=3; day=18; hr=17; min=39; sec=41; ms=23; ]

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Application No: 10573229

Version No: 2.1

Input Set:

Output Set:

Started: 2008-03-18 17:38:08.824

Finished: 2008-03-18 17:38:16.531

Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 707 ms

Total Warnings: 134

Total Errors: 0

No. of SeqIDs Defined: 312

Actual SeqID Count: 312

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**Input Set:**

**Output Set:**

**Started:** 2008-03-18 17:38:08.824  
**Finished:** 2008-03-18 17:38:16.531  
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**Total Warnings:** 134  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 312  
**Actual SeqID Count:** 312

Error code

Error Description

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TURECI, Ozlem  
SAHIN, Ugur  
HELFTENBEIN, Gerd  
SCHLUTER, Volker

<120> Identification of Tumour-Associated Cell Surface Antigens  
for Diagnosis and Therapy

<130> VOS-203

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<141> 2008-03-06

<150> PCT/EP2004/010697

<151> 2004-09-23

<150> DE 103 44 799.7

<151> 2003-09-26

<160> 312

<170> PatentIn Version 3.1

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Thr Pro Gly Glu Ala Gly Lys Ala Pro Leu Phe Gln Gly Phe Arg Ala

35 40 45

Pro Pro Gly Pro Gly Ala Ser Ile Ser Cys Ala Leu Gly Ser Gly Leu

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Ser Phe Tyr Leu Val Thr Phe Leu Gly Asn Gly Gly Met Ile Ile Leu  
35 40 45

Ile Gln Val Asp Ala Gln Leu His Thr Pro Val Tyr Phe Phe Leu Ser  
50 55 60

His Leu Ala Phe Leu Asp Ala Cys Cys Ala Ser Val Ile Thr Pro Gln  
65 70 75 80

Ile Leu Ala Thr Leu Ala Thr Asp Lys Thr Val Ile Ser Tyr Gly Cys  
85 90 95

Arg Ala Val Gln Phe Ser Phe Phe Thr Ile Cys Ala Gly Thr Glu Cys  
100 105 110

Tyr Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Ser Asn  
115 120 125

Pro Leu His Cys Asn Met Thr Met Thr Pro Gly Thr Cys Arg Val Phe  
130 135 140

Leu Ala Ser Ala Phe Ile Cys Gly Val Ser Gly Ala Ile Leu His Thr  
145 150 155 160

Thr Cys Thr Phe Thr Leu Ser Phe Cys Cys Asp Asn Gln Ile Asn Phe  
165 170 175

Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Ser Met  
180 185 190

Thr Gln Thr Glu Ile Val Ile Leu Leu Cys Ala Lys Cys Met Phe Leu  
195 200 205

Ala Asn Val Met Val Ile Leu Ile Cys Tyr Met Leu Ile Ile Arg Ala  
210 215 220



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Gly	Ser	Gly	Lys	Ala	Val	Gly	Trp	Ser	Trp	Arg	Ser	Leu	Arg	Glu	Thr	260	265	270	
Asn	His	Met	Arg	Pro	Gly	Asn	Thr	Ser	Lys	His	Ser	Ala	Ala	Gln	Leu	275	280	285	
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Arg	Cys	Gly	Trp	Glu	Gly	His	Pro	Ser	His	Ser	Tyr	Thr	Leu	Gly	Leu	370	375	380	
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Gly	Pro	Pro	Ala	Thr	Cys	Gln	Arg	Pro	Asp	Leu	Gln	Thr	Pro	Ser	Pro	405	410	415	
Pro	Lys	Glu	Ile	Cys	Ser	Ser	Gly	Leu	Arg	Pro	Leu	Thr	His	Ser	Ala	420	425	430	
Gly	Pro	Asp	Arg	Ser	Gln	Val	Pro	Ala	Ala	Ser	Gly	Ala	Ala	Thr	Met	435	440	445	

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450 455 460

Ser Cys Ile Ser Gly Ile Gln Ala Leu Gly Ser Thr Leu Ala Leu Leu  
465 470 475 480

Ser Asn Gln Leu Pro Pro Thr Thr Asn Tyr Ala Cys Gly Ser Gln Gln  
485 490 495

His Leu Leu Gly Val Val Gly Gly Met Thr Phe Leu Glu Ser Glu Pro  
500 505 510

Met Ser Glu Leu Leu Ser Ile Tyr Arg Val Pro Gln Gly Gln Arg Leu  
515 520 525

Thr Lys Asn Phe Glu Val Lys Glu Leu Val Cys Thr Tyr Leu Val Gly  
530 535 540

Gln Leu Pro Tyr Gly Leu Val Ser Tyr Asp Asn Ser Asn Phe Glu Trp  
545 550 555 560

Leu Asp Gln Gln Leu Gln Lys Gln Ile Gly Gly Glu Gly Leu Pro Val  
565 570 575

Gly Ala Ala Pro Ser Arg Val Ala Arg Gln Gln Ser Asp Glu Glu Ala  
580 585 590

Val Gly Gly Val Gln Gly Tyr Arg Trp Ser Gly Leu Gly Ala Ser Ile  
595 600 605

Gln Ser Ala Arg Glu Gly Ala Trp His Arg Thr Gly Leu Glu Asn Met  
610 615 620

Thr Thr Ala His Leu Ser Ala Phe Lys Leu Pro Asp Leu Thr Ala Thr  
625 630 635 640

Tyr Gln Ala Tyr Leu Ala Ala Lys Ala Leu Trp Val Ala Tyr Gln Asn  
645 650 655

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675

680

685

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Phe Asp Ile Lys Asn Ile Tyr Val Leu Pro Asp Leu Ser Gly Gln Thr  
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Ala Ile Val Gly His Phe Asp Phe Arg Ala Pro Ser Gly Lys Glu Leu  
725 730 735

Leu Leu Asp Asp Ser Ala Ile Val Trp Ala Glu Gly Pro Leu Lys Ile  
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Arg Ala Glu Arg Thr Leu Arg Thr Lys Thr Thr Gln His Leu Ser His  
755 760 765

Pro Lys Leu Gln Glu Ser Leu Pro Leu Ser Ala Thr Lys Asn Val Leu  
770 775 780

Trp Lys Pro Gly Ser Gln Pro Tyr Leu Arg Ser Gln Asn Ala Ala Thr  
785 790 795 800

Lys Ala Phe Pro Asp Pro Glu Glu Lys Ser Gln Cys His Gln Phe Leu  
805 810 815

Phe Leu Pro Ser Asp Ser Val Ala Cys Gln Lys Cys Ser Asp Asn Gln  
820 825 830

Trp Pro Asn Val Gln Lys Gly Glu Cys Ile Pro Lys Thr Leu Asp Phe  
835 840 845

Leu Phe Tyr His Lys Pro Leu Asp Thr Ala Leu Ala Val Cys Thr Ala  
850 855 860

Leu Leu Phe Leu Leu Ala Leu Ala Ile Leu Gly Ile Phe His Val Val  
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Cys Ser Cys Val Trp Val Ser Phe Ile Pro Ala His Met His Ala His  
885 890 895

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900 905 910

Gly Gly Leu Met Ser Ser Leu Phe Phe Ser Lys Cys Tyr Ile Ile Leu  
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Ser Asn Ser Thr Ala Leu Ala Leu Val Arg Pro Ser Ser Ser Gly Leu  
 35 40 45

Ile Asn Ser Asn Thr Asp Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg  
 50 55 60

Asp Ile Leu Asn Asn Phe Pro His Ser Ile Ala Arg Gln Lys Arg Ile  
 65 70 75 80

Leu Val Asn Leu Ser Met Val Glu Asn Lys Leu Val Glu Leu Glu His  
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Thr

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